In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 10, line 1-9, and replace it with the following paragraph:

Figure 1B shows alignment of partial 16S rRNA sequences of Staphylococcus schleiferi (GenBank accession number AB009945) **(SEQ ID NO: 5)**, Staphylococcus schleiferi (GenBank accession number 83372) **(SEQ ID NO: 6)**, Staphylococcus schleiferi (GenBank accession number S83568) **(SEQ ID NO: 7)**, Staphylococcus schleiferi (GenBank accession number Z26904) **(SEQ ID NO: 8)**, Staphylococcus aureus (GenBank accession number Y15856) **(SEQ ID NO: 9)**, Staphylococcus aureus (GenBank accession number AF076030) **(SEQ ID NO: 10)**. Differences between nucleobase sequences of Staphylococcus aureus and corresponding nucleobase sequences of Staphylococcus schleiferi are indicated by characters in bold over shaded boxes. Notice that the upper two strains of Staphylococcus schleiferi differ from the lower two strains by one base.

Please delete the paragraph on page 10, lines 11-22, and replace it with the following paragraph:

In Figure 1A, the anti-parallel hybridization of the probe nucleobase sequence GCT-TCT-CGT-CCG-TTC **(SEQ ID NO: 1)** (Probe A) to both the wanted target sequence of Staphylococcus aureus **(SEQ ID NO: 4)** and to the unwanted target sequence of Staphylococcus schleiferi **(SEQ ID NO: 3)** and of the probe nucleobase sequence ACT-TCA-AAG-GAG-CAA **(SEQ ID NO: 2)** (Probe B) to the adjacent, unwantedtarget sequence of Staphylococcus schleiferi are illustrated. The two nucleobase sequences are labeled with fluorescein (F) and dabcyl (Q), respectively, at adjoining ends. The figure demonstrates how both Probe A and Probe B will bind to the Staphylococcus schleiferi target, but only Probe A will bind to the Staphylococcus aureus target. Note that even though there is a one base mismatch between Probe A probe and the Staphylococcus schleiferi target sequence, a relatively stabile hybrid is formed. This stability is due in part to the total length of the probe

(15 bases), and to the relatively high stability of G-T pairs (mismatches) as compared to all other PNA-NA mismatch hybrids

Please delete the paragraph on page 18, line 8-12, and replace it with the following paragraph:

For example, the Probe A can include the following nucleotide sequence: GCT-TCT-CGT-CCG-TTC **(SEQ ID NO: 1)** and/or the Probe B can include the following nucleotide sequence: ACT-TCA-AAG-GAG-CAA **(SEQ ID NO: 2)**. In this embodiment, the probes can include other nucleobases (eg., less than about 10, preferably less than about 5, usually one or two nucleobases), provided such additions do not detectably impact function of the probes.

Please delete the paragraph on page 18, lines 14-17, and replace it with the following paragraph:

However, in embodiments in which hybridization specificity is especially important, Probe A can consist essentially of the following nucleotide sequence: GCT-TCT-CGT-CCG-TTC **(SEQ ID NO: 1)** and the first fluorophore and/or the Probe B can consist essentially of the following nucleotide sequence: ACT-TCA-AAG-GAG-CAA **(SEQ ID NO: 2)** and the quencher.

Please delete the paragraph on page 18, lines 19-24, and replace it with the following paragraph:

Where even more potential hybridization specificity is desired, the Probe A can consist of the following nucleotide sequence: GCT-TCT-CGT-CCG-TTC **(SEQ ID NO: 1)** and the fluorophore. Also, the Probe B can consist of the following nucleotide sequence: ACT-TCA-AAG-GAG-CAA **(SEQ ID NO: 2)** and the quencher. In this embodiment, the Probe A is labeled with the fluorophore at the probe terminus closest to the binding site of Probe B, and

Probe B is labeled with a quencher at the probe terminus closest to the binding site of Probe A.

Please delete the paragraph on page 26, lines 22-24, and replace it with the following paragraph:

PNA probe sequence

Probe A Flu-OO- GCT-TCT-CGT-CCG-TTC **(SEQ ID NO: 1)**

Probe B ACT-TCA-AAG-GAG-CAA-Lys-lys(Dabsyl)

Please add the presently submitted Sequence Listing (pages 29-30) and re-number originally filed pages 29-34 to 31-36.